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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/525,885DATE: 04/03/2000
TIME: 11:08:19

Input Set: I525885.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

ENTERED

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1  <110> APPLICANT: Hanson, Andrew D.
2      Nuccio, Michael L.
3      Henry, Susan A.
4  <120> TITLE OF INVENTION: POLYNUCLEOTIDE COMPOSITIONS ENCODING
5      S-ADENOSYL-L-METHIONINE: PHOSPHOETHANOLAMINE
6      N-METHYLTRANSFERASE AND METHODS FOR MODULATING LIPID
7      BIOSYNTHESIS IN PLANTS
8  <130> FILE REFERENCE: 4300.012700
9  <140> CURRENT APPLICATION NUMBER: US/09/525,885
10 <141> CURRENT FILING DATE: 2000-03-15
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO 1
14 <211> LENGTH: 2235
15 <212> TYPE: DNA
16 <213> ORGANISM: Spinacia oleracea
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20      attgccattg agggtcacta atacttttaa ctatctcctt ctttttcttt cccacaattt 180
21      ctgcgttttc acgcacatta atctcaccta ttttctagct tcttcatttt ctcaatcaat 240
22      ctctcgtgtt attatggccg cttcagctat gggagtgttg caagagagag aggtgttcaa 300
23      gaaatactgg attgaacact ctggtgattt gactgttgag gctatgatgc ttgattcaca 360
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25      aggaaagtct gtcttagaac tcggtgctgg tattggtcgt tttactggtg aattggccga 480
26      gaaagctagc caggtcatcg ctctggattt cattgagagt gttataaaga agaataaaga 540
27      cataaatggg cattacaaaa atgtgaagtt tatgtgtgct gatgtgacat ctccaagtct 600
28      caacatttca ccaaatcccg tggatatcat attctccaat tggctactca tgtatctttc 660
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43      atatggcaag atgcttaaa atgctggatt cgttgagggt attgctgaga ataggactga 1560
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47      aatgagctgg tgaaagcagc acggtgcctt tttctagtat tagtttatca atgtattttc 1800
48      agttcatgga ctgtatatgc aaaatctacc aataagctgt gagttgcaaa ctgaaagatg 1860
49      atttcttata gtcacttctg aattagcaca agcagtgaag ttcgcataag aaactgaagg 1920
50      gaactcatgg agttgcagac gaaatcatca aaacggcaga acccactctc tatatagaga 1980
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53      taatgtgtat tagtttggtg aaagtgaac ttgcaacaca cttattcaca agtgtgtagg 2160
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58 <212> TYPE: PRT

59 <213> ORGANISM: Spinacia oleracea

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64      20              25              30
65      Leu Asp Ser Gln Ala Ser Asp Leu Asp Lys Val Glu Arg Pro Glu Val
66      35              40              45
67      Leu Ser Met Leu Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly
68      50              55              60
69      Ala Gly Ile Gly Arg Phe Thr Gly Glu Leu Ala Glu Lys Ala Ser Gln
70      65              70              75              80
71      Val Ile Ala Leu Asp Phe Ile Glu Ser Val Ile Lys Lys Asn Glu Ser
72      85              90              95
73      Ile Asn Gly His Tyr Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr
74      100             105             110
75      Ser Pro Ser Leu Asn Ile Ser Pro Asn Ser Val Asp Ile Ile Phe Ser
76      115             120             125
77      Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu Glu Val Glu Arg Leu Val
78      130             135             140
79      Glu Arg Met Leu Lys Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg
80      145             150             155             160
81      Glu Ser Cys Phe His Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro
82      165             170             175
83      Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys Glu Cys
84      180             185             190
85      His Met Gln Asp Asp Ser Gly Asn Ser Tyr Glu Leu Ser Leu Ile Gly
86      195             200             205
87      Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln Asn Gln
88      210             215             220
89      Ile Ser Trp Leu Trp Gln Lys Val Asp Ser Glu Asp Asp Lys Gly Phe
90      225             230             235             240
91      Gln Arg Phe Leu Asp Ser Ser Gln Tyr Lys Phe Asn Ser Ile Leu Arg
92      245             250             255
93      Tyr Glu Arg Val Phe Gly Pro Gly Tyr Val Ser Thr Gly Gly Leu Glu
94      260             265             270

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97      Val Leu Asp Val Gly Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala
98              290                      295                      300
99      Glu Asn Tyr Asp Val Glu Val Val Gly Ile Asp Leu Ser Ile Asn Met
100     305                      310                      315                      320
101     Ile Ser Phe Ala Leu Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu
102              325                      330                      335
103     Phe Glu Val Ala Asp Cys Thr Lys Lys Asp Tyr Pro Glu Asn Ser Phe
104              340                      345                      350
105     Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro
106              355                      360                      365
107     Ala Leu Phe Arg Ser Phe His Lys Trp Leu Lys Pro Gly Gly Lys Val
108              370                      375                      380
109     Leu Ile Ser Asp Tyr Cys Lys Ser Ala Gly Thr Pro Ser Ala Glu Phe
110     385                      390                      395                      400
111     Ala Ala Tyr Ile Arg Gln Arg Gly Tyr Asp Leu His Asp Val Lys Ala
112              405                      410                      415
113     Tyr Gly Lys Met Leu Lys Asp Ala Gly Phe Val Glu Val Ile Ala Glu
114              420                      425                      430
115     Asn Arg Thr Asp Gln Phe Ile Gln Val Leu Gln Lys Glu Leu Asp Ala
116              435                      440                      445
117     Leu Glu Gln Glu Lys Asp Asp Phe Ile Asp Asp Phe Ser Glu Glu Asp
118              450                      455                      460
119     Tyr Asn Asp Ile Val Asp Gly Trp Lys Ala Lys Leu Val Arg Thr Thr
120     465                      470                      475                      480
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122              485                      490
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130 attgccattg agggtcacta atacttttaa ctatctcctt ctttttcttt ccacaaattt 180
131 ctgcgttttc acgcacatta atctcaccta ttttctagct tcttcatttt ctcaatcaat 240
132 ctctcgtggtt attatggccg ctccagctat gggagtgttg caagagagag aggtgttcaa 300
133 gaaatactggg attgaacact ctgttgattt gactgttgag gctatgatgc ttgattcaca 360
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136 gaaagctagc caggctcatcg ctctggattt cattgagagt gttataaaga agaatgaaag 540
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139 tgatgaagag gttgagcgtc tggttgaaag gatgttgaaa tggttgaagc caggaggata 720
140 cattttcttc agagaatctt gttttcatca atcaggagat cacaagcgca aaagcaatcc 780
141 aaccctactac cgtgaaccta gggttctcac caagatcttc aaagaatgcc atatgcaaga 840
142 tgattctggg aactcctatg agctctccct aattggctgc aaatgtattg gagcttatgt 900
143 caaaaagcaag aagaatcaga accagataag ctgggttatgg cagaaagttg attcagagga 960
144 tgacaagggg ttccagcgat tcttggtatc tagtcaatac aagtttaaca gcatactgcg 1020

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155      20          25          30
156      Leu Asp Ser Gln Ala Ser Asp Leu Asp Lys Val Glu Arg Pro Glu Val
157      35          40          45
158      Leu Ser Met Leu Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly
159      50          55          60
160      Ala Gly Ile Gly Arg Phe Thr Gly Glu Leu Ala Glu Lys Ala Ser Gln
161      65          70          75          80
162      Val Ile Ala Leu Asp Phe Ile Glu Ser Val Ile Lys Lys Asn Glu Ser
163      85          90          95
164      Ile Asn Gly His Tyr Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr
165      100         105         110
166      Ser Pro Ser Leu Asn Ile Ser Pro Asn Ser Val Asp Ile Ile Phe Ser
167      115         120         125
168      Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu Glu Val Glu Arg Leu Val
169      130         135         140
170      Glu Arg Met Leu Lys Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg
171      145         150         155         160
172      Glu Ser Cys Phe His Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro
173      165         170         175
174      Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys Glu Cys
175      180         185         190
176      His Met Gln Asp Asp Ser Gly Asn Ser Tyr Glu Leu Ser Leu Ile Gly
177      195         200         205
178      Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln Asn Gln
179      210         215         220
180      Ile Ser Trp Leu Trp Gln Lys Val Asp Ser Glu Asp Asp Lys Gly Phe
181      225         230         235         240
182      Gln Arg Phe Leu Asp Ser Ser Gln Tyr Lys Phe Asn Ser Ile Leu Arg
183      245         250         255
184      Tyr Glu Arg Val Phe Gly Pro Gly Tyr Val Ser Thr Gly Gly Leu Glu
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190 <211> LENGTH: 11
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

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